Amendments to the Specification:

Please replace paragraph [0018], referring to the published application US 20060160991, with the following amended paragraph:

-- On the other hand, in a preferred embodiment, the PCOTH polypeptide consists of a putative 100 amino acid sequence set forth in SEQ ID NO: 2 (GenBank® Accession No. AB113650). PCOTH is encoded by the open reading frame of SEQ ID NO: 1 and comprises a collagen triple helix repeat (FIG. 1(C)). The present application also provides an isolated protein encoded from at least a portion of the PCOTH polynucleotide sequence, or polynucleotide sequences at least 30% and more preferably at least 40% complementary to the sequence set forth in SEQ ID NO: 1 (LOC221179(XO__167995) ~~(XP__167955)~~). --

Please replace paragraph [0034] with the following amended paragraph:

-- FIG. 1(A) depicts photographs showing the result of validation of over-expression of D4493 (PCOTH) in prostate cancer cells by RT-PCR. The microdissected normal prostate duct epithelial cells (N) and prostate cancer cells (T) from the same individual were compared by semiquantitative RT-PCR. ACTB was used for normalization of the results. (B) depicts photographs showing the result of Northern blot analysis of normal human multiple tissues. High and localized expression in testis and prostate and minor expression in heart and bone marrow were detected. (C) depicts the amino acid sequence of D4493 (PCOTH) product (SEQ ID NO:2). The product consists of 100 amino acids and has collagen triple helix repeats which is characterized by the G-X-X motif repeat. G is glycine and X is preferrably proline. --

Please replace paragraph [0068] with the following amended paragraph:

-- According to the present invention another gene, PCOTH, was also identified to be specifically over-expressed in prostate cancer cells compared to corresponding non-cancerous tissues. The identified gene was identical with LOC221179 (XO__167995) ~~(XP__167955)~~. However, the PCOTH gene was revealed to encode a 100-amino acid protein set forth in SEQ ID

NO: 2 (GenBank® Accession No. AB113650) encoded by the open reading frame consisting of 300 nucleotides shown in SEQ ID NO: 1 which differed from that known for LOC221179 (XO__167995) ~~(XP__167955)~~. PCOTH was shown to comprise a collagen triple helix repeat and its exogenous product was localized in the cell membrane (FIG. 1). Therefore, the gene was dubbed "prostate collagen triple helix".

Please replace paragraph [0103] with the following amended paragraph:

-- For example, measurement of absorbance, enzyme-linked immunosorbent assay (ELISA), enzyme immunoassay (EIA), radioimmunoassay (RIA) and/or immunofluorescence maybe used to measure the antigen binding activity of the antibody of the invention. In ELISA, the antibody of the present invention is immobilized on a plate, a polypeptide of the invention is applied to the plate, and then a sample containing a desired antibody, such as culture supernatant of antibody producing cells or purified antibodies, is applied. Then, a secondary antibody that recognizes the primary antibody and is labeled with an enzyme, such as alkaline phosphatase, is applied, and the plate is incubated. Next, after washing, an enzyme substrate, such as p-nitrophenyl phosphate, is added to the plate, and the absorbance is measured to evaluate the antigen binding activity of the sample. A fragment of the polypeptide, such as a C-terminal or N-terminal fragment, may be used as the antigen to evaluate the binding activity of the antibody. BIAcore® (Pharmacia) may be used to evaluate the activity of the antibody according to the present invention. --

Please replace paragraph [0114] with the following amended paragraph:

-- The nucleotide sequence of siRNAs may be designed using an siRNA design computer program available from the Ambion® website on the world wide web at ~~(http://www.~~ ambion.com/techlib/misc/siRNA_finder.html~~)~~. Nucleotide sequences for the siRNA are selected by the computer program based on the following protocol. --

Please replace paragraph [0117] with the following amended paragraph:

-- 2. Compare the potential target sites to the human genome database and eliminate from consideration any target sequences with significant homology to other coding sequences. The homology search can be performed using BLAST, which can be found on the NCBI server on the world wide web at: ~~www.~~ ncbi.nlm.nih.gov/BLAST/. --

Please replace paragraph [0118] with the following amended paragraph:

-- 3. Select qualifying target sequences for synthesis. At Ambion®, preferably several target sequences can be selected along the length of the gene for evaluation. --

Please replace paragraph [0151] with the following amended paragraph:

-- A biosensor using the surface plasmon resonance phenomenon may be used as a mean for detecting or quantifying the bound compound in the present invention. When such a biosensor is used, the interaction between the polypeptide of the invention and a test compound can be observed real-time as a surface plasmon resonance signal, using only a minute amount of polypeptide and without labeling (for example, BIAcore®, Pharmacia). Therefore, it is possible to evaluate the binding between the polypeptide of the invention and a test compound using a biosensor such as BIAcore®. --

Please replace paragraph [0177] with the following amended paragraph:

-- In the present invention, a biosensor using the surface plasmon resonance phenomenon may be used as a mean for detecting or quantifying the bound protein. When such a biosensor is used, the interaction between the proteins can be observed real-time as a surface plasmon resonance signal, using only a minute amount of polypeptide and without labeling (for example, BIAcore®, Pharmacia). Therefore, it is possible to evaluate the binding between the MICAL2-PV polypeptide and actin using a biosensor such as BIAcore®. --

Please replace paragraph [0257] with the following amended paragraph:

-- Gene-expression profiles of purified cancer cells from 20 prostate cancers were analyzed using cDNA microarray representing 23,040 human genes. As a result, 88 genes that were commonly up-regulated in prostate cancer cells were identified. Among the identified genes, one gene with an in-house code D4493 that was markedly up-regulated in more than 50% of prostate cancer was focused and validated for its over-expressed pattern in prostate cancer cells by RT-PCR (FIG. 1A). D4493 was overlapped by two ESTs (BC015452 and BG178505) derived from ~~form~~ prostate cancer cDNA library and was revealed to be identical with LOC221179 (XP__167995) ~~(XP_167955)~~. Comparison between mouse/rat genome sequences, a novel coding region of LOC221179 was determined which codes a 100-amino acid protein. Northern blot analysis demonstrated that LOC221179 was highly and locally expressed in prostate and testis (FIG. IB). This product has one characteristic domain, collagen triple helix repeat (FIG. 1C), which is a characteristic feature of the collagen superfamily. Thus, the gene was dubbed "PCOTH (prostate collagen triple helix)". --